

# SEQUENCE LISTING

<110> Allen, Stephen M.  
Kinney, Anthony J.

<120> CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE

<130> BB1145 US NA

<140> 09/644,907

<141> 2000-08-24

<150> 60/076,203

<151> 1998-02-27

<160> 11

<170> Microsoft Word Version 7.0A

<210> 1

<211> 1314

<212> DNA

<213> Zea mays

<400> 1

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tttcaagcta gtgctgggaa agaatctcaa atacagttcc tgctatttcc ctggtgattc   420
aagcacccta gaagatgctg aggttgcgat gatggatctg tattgtgaga ggtcgaaact   480
acaagatggc caaagtatcc tagatggttg atgtggatgg ggatcccttt cactgtacat   540
tgcaaagaaa tataggaact gcagtgtaac agggatatgc aactctacta cacagaaggc   600
ttttatagaa gagcaatgta gggataacga gctgtcaaat attgagataa tcgtagccga   660
catcagcaag tttgagatgg agcgtctctt tgacaggatc gtatctatag agatgtttga   720
gcacatgaaa aactacaagt cgcttcttaa gaagatatcc aggtggatga aagaggatgg   780
cctactattc gttcacctct tctgccacaa agcatttcca tatcactttg aggataaaaa   840
cgatgatgac tggatcacga ggtatttctt cactggagga acaatgccat ctgcaaacct   900
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ttatgctaga actagcgagg agtggctaaa acgtatggac aagagcatca cttcaataag  1020
gctgatcttc gaggaactt atgggaagga atcgactacc aaatggatag cttattggcg  1080
gacgttcttc atctcggtag ctgaactttt tggatacaac aatggagatg aatggatggt  1140
tgcccattac ttgttccgaa agaagtagag gctactgctt ggaagtaccc aatcaaaaat  1200
caatgttttc agtaattttg tcatgtacat cgacgaacaa ctccttttct ggcacgtagt  1260
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<210> 2

<211> 385

<212> PRT

<213> Zea mays

<400> 2

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Ser Val Ala Glu Arg Ala Tyr Glu Ala Ala Thr Arg Ser Ala Leu Val

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35					40					45					
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65					70					75					80
Pro	Leu	Gln	Leu	Gln	Gln	Leu	Leu	Gln	Phe	Val	His	Ser	Leu	Glu	Glu
				85					90					95	
Met	Pro	Ile	Ala	Ile	Glu	Thr	Asp	Lys	Ala	Lys	Ala	Gln	His	Tyr	Glu
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Leu	Pro	Thr	Thr	Phe	Phe	Lys	Leu	Val	Leu	Gly	Lys	Asn	Leu	Lys	Tyr
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Ser	Ser	Cys	Tyr	Phe	Pro	Gly	Asp	Ser	Ser	Thr	Leu	Glu	Asp	Ala	Glu
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Val	Ala	Met	Met	Asp	Leu	Tyr	Cys	Glu	Arg	Ser	Lys	Leu	Gln	Asp	Gly
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Gln	Ser	Ile	Leu	Asp	Val	Gly	Cys	Gly	Trp	Gly	Ser	Leu	Ser	Leu	Tyr
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Ile	Ala	Lys	Lys	Tyr	Arg	Asn	Cys	Ser	Val	Thr	Gly	Ile	Cys	Asn	Ser
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		195					200					205			
Ser	Asn	Ile	Glu	Ile	Ile	Val	Ala	Asp	Ile	Ser	Lys	Phe	Glu	Met	Glu
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Arg	Ser	Phe	Asp	Arg	Ile	Val	Ser	Ile	Glu	Met	Phe	Glu	His	Met	Lys
225					230					235					240
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Gly	Leu	Leu	Phe	Val	His	Leu	Phe	Cys	His	Lys	Ala	Phe	Pro	Tyr	His
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Gly	Gly	Thr	Met	Pro	Ser	Ala	Asn	Leu	Leu	Leu	Tyr	Phe	Gln	Glu	Asp
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Val	Ser	Val	Val	Asp	His	Trp	Leu	Val	Ser	Gly	Thr	His	Tyr	Ala	Arg
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Thr	Ser	Glu	Glu	Trp	Leu	Lys	Arg	Met	Asp	Lys	Ser	Ile	Thr	Ser	Ile
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Arg	Leu	Ile	Phe	Glu	Glu	Thr	Tyr	Gly	Lys	Glu	Ser	Thr	Thr	Lys	Trp
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Ile	Ala	Tyr	Trp	Arg	Thr	Phe	Phe	Ile	Ser	Val	Ala	Glu	Leu	Phe	Gly
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Lys  
 385

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 <212> DNA  
 <213> Phaseolus lunatus

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 cttgcatatg acgctacggt gaagctcatg ctgtctgcac tcgagcgcaa cctgctacct 180  
 gacgccgtca ccaggagact cacgcgcata cttttggcta ctgccttcg ctcttcttcc 240  
 aacacatcct cggatcttca gctttcacac ctccaacatt tcgcacattc tttaacaagag 300  
 atgcccatag caatcaacac tgagaagccg aaatctcaac attatgaatt accaacagct 360  
 ttcttcaagc tcgtccttgg aagcaatctc aaatacagct gttgctatct ctcttctgcc 420  
 tcaatgacgc tggaagatgc tgaagaagca atggtgaaac tgtactgcga gagatcaaac 480  
 ctcacagatg gtcatacagt acttgatgtg ggatgtgggt ggggatcgct agctttaaac 540  
 attcccaaga attacactaa ctgcagaggt acaggaatct gcaattctac aactcaaaag 600  
 gcttatattg aggagaagt cggggatctt cagctgcaaa atatgaatat tatagttgct 660  
 gatattagca cgttggaagt ggaagcttct tatgacagaa tattttccat agaaatggtt 720  
 gagcatatga agaactacaa agagcttctc aagaagatat ccaaattggat gaaagaggat 780  
 agccttttat ttgtgcatta cttctgccac aaagcatttg cctaccactt tgaggacaaa 840  
 aatgaagatg actggattac aagatacttc ttttctggag gaactatgcc gtcagcaaat 900  
 ctacttcttt attttcaaga tgatgttaca gtcacaaacc attggctagt aaatgggaaa 960  
 cactactcac aaaccagtga agaattggctt aaaagaatgg accagagaat gacttacatc 1020  
 aagccaatta tgcaatcaac ttatggcaat gattcagcaa ccaagtggac tgcctattgg 1080  
 agaacattct tcatatctgt agcggaaact ttcggataca ataacgggtg agaattggatg 1140  
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 aacctgccaa tcgaagttgc aatttcaata atggttgta cttaattaat ttagtttaat 1320  
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 atctatttat atataaaaaa aaaaaaaaaa aa 1412

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 <211> 355  
 <212> PRT  
 <213> Phaseolus lunatus

<400> 4  
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 Leu Thr Arg Ile Leu Leu Ala Thr Arg Leu Arg Ser Ser Ser Asn Thr  
 35 40 45  
 Ser Ser Asp Leu Gln Leu Ser His Leu Gln His Phe Ala His Ser Leu  
 50 55 60  
 Gln Glu Met Pro Ile Ala Ile Asn Thr Glu Lys Pro Lys Ser Gln His  
 65 70 75 80  
 Tyr Glu Leu Pro Thr Ala Phe Phe Lys Leu Val Leu Gly Ser Asn Leu  
 85 90 95

Lys Tyr Ser Cys Cys Tyr Phe Ser Ser Ala Ser Met Thr Leu Glu Asp  
 100 105 110  
 Ala Glu Glu Ala Met Leu Lys Leu Tyr Cys Glu Arg Ser Asn Leu Thr  
 115 120 125  
 Asp Gly His Thr Val Leu Asp Val Gly Cys Gly Trp Gly Ser Leu Ala  
 130 135 140  
 Leu Asn Ile Pro Lys Asn Tyr Thr Asn Cys Arg Val Thr Gly Ile Cys  
 145 150 155 160  
 Asn Ser Thr Thr Gln Lys Ala Tyr Ile Glu Glu Lys Cys Arg Asp Leu  
 165 170 175  
 Gln Leu Gln Asn Met Asn Ile Ile Val Ala Asp Ile Ser Thr Leu Glu  
 180 185 190  
 Met Glu Ala Ser Tyr Asp Arg Ile Phe Ser Ile Glu Met Phe Glu His  
 195 200 205  
 Met Lys Asn Tyr Lys Glu Leu Leu Lys Lys Ile Ser Lys Trp Met Lys  
 210 215 220  
 Glu Asp Ser Leu Leu Phe Val His Tyr Phe Cys His Lys Ala Phe Ala  
 225 230 235 240  
 Tyr His Phe Glu Asp Lys Asn Glu Asp Asp Trp Ile Thr Arg Tyr Phe  
 245 250 255  
 Phe Ser Gly Gly Thr Met Pro Ser Ala Asn Leu Leu Leu Tyr Phe Gln  
 260 265 270  
 Asp Asp Val Thr Val Ile Asn His Trp Leu Val Asn Gly Lys His Tyr  
 275 280 285  
 Ser Gln Thr Ser Glu Glu Trp Leu Lys Arg Met Asp Gln Arg Met Thr  
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 Tyr Ile Lys Pro Ile Met Gln Ser Thr Tyr Gly Asn Asp Ser Ala Thr  
 305 310 315 320  
 Lys Trp Thr Ala Tyr Trp Arg Thr Phe Phe Ile Ser Val Ala Glu Leu  
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<212> DNA

<213> Oryza sativa

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 ggcggcgacg cgcgcggcgc tggcggcgct ggagcgcaac gccctccccg acgcgggtcac 180  
 ccggcgccctg acgcgggtgc tgctcgcgca gcgcctccgc ctccggctacc tcccctcctc 240  
 ctctctctcc gcgccnctcc acctccacca cctcctcctc ttgcccacg ctctagaaga 300  
 gatgcccacg gcaatcgaga cggagaaaagc taaagaccaa gcactacgag ttgcccacga 360  
 catttttcaa gctgggttctt ggaaggaatc tcaagtacag ctcatgttac ttccctgacg 420  
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 <213> Oryza sativa

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<220>  
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 <222> (118)  
 <223> Xaa = ANY AMINO ACID

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 20 25 30  
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 35 40 45  
 Ser Ser Ser Ser Ser Ala Pro Leu His Leu His His Leu Leu Leu Phe  
 50 55 60  
 Ala His Ala Leu Glu Glu Met Pro Ile Ala Ile Glu Thr Glu Lys Ala  
 65 70 75 80  
 Lys Xaa Gln His Tyr Glu Leu Pro Thr Thr Phe Phe Lys Leu Val Leu  
 85 90 95  
 Gly Arg Asn Leu Lys Tyr Ser Ser Cys Tyr Phe Pro Asp Glu Ser Ser  
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 Thr Leu Glu Asp Ala Xaa Val  
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 gtgaagctca tgctggctgc actcgaacgc aacgtgctcc ctgacgtcat caccaggaga 180  
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 ggaaacaatc tcaaatacag ctggtgttat ttctcttctg cctcaatgac gctggatgat 420  
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 gtgcttgatg tgggatgcgg ttggggatcg ttggctctat acattgccaa gaattacact 540  
 aactgtaggg ttacaggaat ctgcaattcc acaactcaaa aggcttatat tgaggagaag 600  
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 atggagactt cttatgacag aatattttcc atagaaatgt ttgagcatat gaagaactat 720  
 aaagatcttc tgaagaagat atccaaatgg atgaaagagg atagcctttt atttgttcat 780  
 tacttctgcc acaaagcatt tgcctaccac tttgaggaca aaaatgaaga tgactggatt 840  
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 atgatgttac tgtcacaacc attgggctac taatgg 936

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 <212> PRT  
 <213> Glycine max

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 35 40 45  
 Glu Arg Asn Val Leu Pro Asp Val Ile Thr Arg Arg Leu Thr Arg Leu  
 50 55 60  
 Leu Leu Ala Thr Arg Leu Arg Ser Ala Tyr Lys Pro Ser Ser Gln Leu  
 65 70 75 80  
 Gln Leu Ser Asp Leu Leu Tyr Phe Ala His Ser Leu Gln Glu Met Pro  
 85 90 95  
 Ile Ala Ile Asn Thr Asp Lys Pro Lys Ser Gln His Tyr Glu Leu Pro  
 100 105 110  
 Thr Ala Phe Phe Lys Leu Val Leu Gly Asn Asn Leu Lys Tyr Ser Cys  
 115 120 125  
 Cys Tyr Phe Ser Ser Ala Ser Met Thr Leu Asp Asp Ala Glu Glu Ala  
 130 135 140  
 Met Leu Lys Leu Tyr Cys Glu Arg Ser Asn Leu Lys Asp Gly His Thr  
 145 150 155 160  
 Val Leu Asp Val Gly Cys Gly Trp Gly Ser Leu Ala Leu Tyr Ile Ala

	165		170		175
Lys Asn Tyr Thr Asn Cys Arg Val Thr Gly Ile Cys Asn Ser Thr Thr					
	180		185		190
Gln Lys Ala Tyr Ile Glu Glu Lys Cys Arg Asp Leu Gln Leu Gln Asn					
	195		200		205
Leu Asn Ile Ile Val Ala Asp Ile Ser Thr Phe Glu Met Glu Thr Ser					
	210		215		220
Tyr Asp Arg Ile Phe Ser Ile Glu Met Phe Glu His Met Lys Asn Tyr					
	225		230		235
Lys Asp Leu Leu Lys Lys Ile Ser Lys Trp Met Lys Glu Asp Ser Leu					
	245		250		255
Leu Phe Val His Tyr Phe Cys His Lys Ala Phe Ala Tyr His Phe Glu					
	260		265		270
Asp Lys Asn Glu Asp Asp Trp Ile Thr Arg Tyr Phe Phe Thr Gly Gly					
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Thr Met Pro Ser Ala Asn Leu Leu Leu Tyr					
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 cgcgctggcg gcgctggagc gcaacctcct gcccgacgcg gtcacccggc ggctcacgcg 180  
 cttcctgctc gcgcagcgcc tccgcctcgg cacgctcccc tccgcgccgc tccagctgca 240

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ggacctcttc ctcttcgccc actcacttga aggcattgccc attgccattg aaacggacac 300
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cctcaaatac agctcatgtt acttccccga tgattcaagc accctagaag atgccgaggt 420
tgcaatgttg gagttgtact gtgagagggc gcagctgcaa gatggccaaa gcattctcga 480
tgttggatgt ggatggggat ccctctctgt atacatagca aagaaatata ggaactgcaa 540
tatcacaggg atatgcaact caacaactca aaagggtttt atagaaaagc agtgtaggga 600
aaatgagcta tcaaattgtt agataattgt tgcagacatc agcaagtttg agatggacgt 660
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<210> 10
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<212> PRT
<213> Triticum aestivum

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35          40          45

Leu Pro Ser Ala Pro Leu Gln Leu Gln Asp Leu Leu Leu Phe Ala His
50          55          60

Ser Leu Glu Gly Met Pro Ile Ala Ile Glu Thr Asp Thr Ala Lys Thr
65          70          75          80

Gln His Tyr Glu Leu Pro Thr Thr Phe Phe Lys Leu Val Leu Gly Lys
85          90          95

Asn Leu Lys Tyr Ser Ser Cys Tyr Phe Pro Asp Asp Ser Ser Thr Leu
100         105         110

Glu Asp Ala Glu Val Ala Met Leu Glu Leu Tyr Cys Glu Arg Ala Gln
115         120         125

Leu Gln Asp Gly Gln Ser Ile Leu Asp Val Gly Cys Gly Trp Gly Ser
130         135         140

Leu Ser Val Tyr Ile Ala Lys Lys Tyr Arg Asn Cys Asn Ile Thr Gly
145         150         155         160

Ile Cys Asn Ser Thr Thr Gln Lys Gly Phe Ile Glu Lys Gln Cys Arg
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Glu Asn Glu Leu Ser Asn Val Glu Ile Ile Val Ala Asp Ile Ser Lys
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Phe Glu Met
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<210> 11
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<212> PRT
<213> Escherichia coli

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<400> 11

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 Gly Ser Ala Pro Ala Asp Ile Arg Val Lys Asn Pro Asp Phe Phe Lys  
 35 40 45  
 Arg Val Leu Gln Glu Gly Ser Leu Gly Leu Gly Glu Ser Tyr Met Asp  
 50 55 60  
 Gly Trp Trp Glu Cys Asp Arg Leu Asp Met Phe Phe Ser Lys Val Leu  
 65 70 75 80  
 Arg Ala Gly Leu Glu Asn Gln Leu Pro His His Phe Lys Asp Thr Leu  
 85 90 95  
 Arg Ile Ala Gly Ala Arg Leu Phe Asn Leu Gln Ser Lys Lys Arg Ala  
 100 105 110  
 Trp Ile Val Gly Lys Glu His Tyr Asp Leu Gly Asn Asp Leu Phe Ser  
 115 120 125  
 Arg Met Leu Asp Pro Phe Met Gln Tyr Ser Cys Ala Tyr Trp Lys Asp  
 130 135 140  
 Ala Asp Asn Leu Glu Ser Ala Gln Gln Ala Lys Leu Lys Met Ile Cys  
 145 150 155 160  
 Glu Lys Leu Gln Leu Lys Pro Gly Met Arg Val Leu Asp Ile Gly Cys  
 165 170 175  
 Gly Trp Gly Gly Leu Ala His Tyr Met Ala Ser Asn Tyr Asp Val Ser  
 180 185 190  
 Val Val Gly Val Thr Ile Ser Ala Glu Gln Gln Lys Met Ala Gln Glu  
 195 200 205  
 Arg Cys Glu Gly Leu Asp Val Thr Ile Leu Leu Gln Asp Tyr Arg Asp  
 210 215 220  
 Leu Asn Asp Gln Phe Asp Arg Ile Val Ser Val Gly Met Phe Glu His  
 225 230 235 240  
 Val Gly Pro Lys Asn Tyr Asp Thr Tyr Phe Ala Val Val Asp Arg Asn  
 245 250 255  
 Leu Lys Pro Glu Gly Ile Phe Leu Leu His Thr Ile Gly Ser Lys Lys  
 260 265 270  
 Thr Asp Leu Asn Val Asp Pro Trp Ile Asn Lys Tyr Ile Phe Pro Asn  
 275 280 285  
 Gly Cys Leu Pro Ser Val Arg Gln Ile Ala Gln Ser Ser Glu Pro His  
 290 295 300  
 Phe Val Met Glu Asp Trp His Asn Phe Gly Ala Asp Tyr Asp Thr Thr  
 305 310 315 320  
 Leu Met Ala Trp Tyr Glu Arg Phe Leu Ala Ala Trp Pro Glu Ile Ala

				325					330					335					
Asp	Asn	Tyr	Ser	Glu	Arg	Phe	Lys	Arg	Met	Phe	Thr	Tyr	Tyr	Leu	Asn				
			340					345					350						
Ala	Cys	Ala	Gly	Ala	Phe	Arg	Ala	Arg	Asp	Ile	Gln	Leu	Trp	Gln	Val				
		355					360					365							
Val	Phe	Ser	Arg	Gly	Val	Glu	Asn	Gly	Leu	Arg	Val	Ala	Arg						
	370					375					380								